



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANTS: Yuan Min Wu and Eileen Xiao-Feng Nie
(ii) TITLE OF THE INVENTION: SOLUTION HYBRIDIZATION OF
NUCLEIC ACIDS WITH ANTISENSE
PROBES HAVING MODIFIED BACKBONES

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Caesar, Rivise, Bernstein, Cohen & Pokotilow, Ltd.
(B) STREET: 12th Floor, 7 Penn Center, 1635 Market Street
(C) CITY: Philadelphia
(D) STATE: Pennsylvania
(E) COUNTRY: U.S.A.
(F) ZIP: 19103-2212

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Tener, David M.
(B) REGISTRATION NUMBER: 37,054
(C) REFERENCE/DOCKET NUMBER: E1047/20006

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 215-567-2010
(B) TELEFAX: 215-751-1142

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
(B) TYPE: nucleotide
(C) STRANDEDNESS: double-stranded
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTCGAGATG TTCCGAGAGC TGAATGAGGC CTTGGAATC 40

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
(B) TYPE: nucleotide
(C) STRANDEDNESS: double-stranded

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTCGAGATG TTCCGAGAGC AGAATGAGGC CTTGGAATC 40

(2) INFORMATION FOR SEQ ID NO:3:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTCGAGATG TTCCGAGAGG AGAATGAGGC CTTGGAATC 40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 40 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTCGAGATG TTCCGAGAGT ACAATGAGGC CTTGGAATC 40

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 40 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACCACTGG 40

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 150 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACCACTGG ATGGAGAATA TTTCACCCTT 60

43

CAGATCCGTG GCGGTGAGCG CTCGAGATG TTCCGAGAGC TGAATGAGGC CTTGGAAGTC 120
AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 150

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACCACTGG ATGGAGAATA TTTCACCCTT 60
CAGATCCGTG GCGGTGAGCG CTCGAGATG TTCCGAGAGC AGAATGAGGC CTTGGAAGTC 120
AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 150

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACCACTGG ATGGAGAATA TTTCACCCTT 60
CAGATCCGTG GCGGTGAGCG CTCGAGATG TTCCGAGAGA AGAATGAGGC CTTGGAAGTC 120
AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 150

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCAACTGGC CAAGACCTGC CCTGTGCAGC TGTGGGTTGA TTCCACACCC CCGCCCGGCA 60
CCCGCGTCCG CGCCATGGCC ATCTACAAGC AGTCACAGCA CATGACGGAG GTTGTGAGGC 120

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases

44

- (B) TYPE: nucleotide with four methylphosphonate
substitutions along its backbone
- (C) STRANDEDNESS: single-stranded
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCTCATTTCAG CTCTCGGA 18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: nucleotide with nine methylphosphonate
substitutions along its backbone
- (C) STRANDEDNESS: single-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTCATTTCAG CTCTCGGA 18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: nucleotide with 15 methylphosphonate
substitutions along its backbone
- (C) STRANDEDNESS: single-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCATTTCAGC TCTCG 15